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Editorial: Adaptation and evolution in marine extreme environments

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Editorial on the Research Topic

Adaptation and evolution in marine extreme environments

Extreme marine environments provide natural laboratories for investigating the limits of life and the mechanisms that allow organisms to persist under challenging conditions (Parrilli et al., 2021; Smith et al., 2025). From the intense ultraviolet radiation experienced in shallow waters to the low temperatures and seasonal constraints of polar ecosystems, the high pressure and darkness of the deep sea, and the steep chemical gradients surrounding hydrothermal vents, marine organisms are exposed to environmental conditions that can strongly constrain survival, growth, reproduction, and ecological interactions (Minic, 2009; Peck, 2018). Yet these environments are not devoid of life (Saeedi, 2026). On the contrary, they support diverse and often highly specialized communities, in which organisms have evolved a remarkable range of physiological, biochemical, morphological, and ecological strategies (Avila et al., 2008; Sánchez et al., 2024). Adaptation to extreme conditions can involve changes at multiple levels of biological organization, from the production and distribution of protective metabolites and modifications of cellular processes, to interactions among hosts, microbial symbionts, viruses, and other members of the community (Hourdez and Lallier, 2007; Núñez-Pons et al., 2018; Pita et al., 2018). Understanding these mechanisms is therefore essential not only for explaining how organisms persist in environments close to physiological limits, but also for understanding how biodiversity is generated and maintained across environmental gradients.

Recent advances in molecular, genomic, and experimental approaches are providing new opportunities to investigate these processes (Guo et al., 2026). The combination of field observations with high-throughput sequencing, metabolomics, phylogenetics, and controlled environmental experiments makes it increasingly possible to connect environmental conditions with the mechanisms underlying adaptation and evolutionary change (Thangaraj and Sun, 2025). Importantly, these approaches reveal that adaptation to extreme environments is not necessarily a property of individual organisms alone. Complex associations

among hosts and their microbial partners can contribute to nutrient acquisition, detoxification, protection from environmental stress, and maintenance of physiological stability. At the same time, environmental extremes can destabilize these associations, potentially reshaping the composition and functioning of entire holobionts (Pita et al., 2018). Evolutionary responses can also be expressed through changes in dispersal and population connectivity, developmental trajectories, morphological traits, and the emergence of cryptic genetic diversity (Burraco et al., 2025; Saeedi, 2026). Exploring these different levels of organization is particularly relevant in the context of ongoing global change, as environmental conditions that were once spatially or temporally restricted may become increasingly widespread or intense.

The contributions gathered in this Research Topic illustrate this diversity of mechanisms and perspectives. They span contrasting environments, from Antarctic and Mediterranean waters to tropical reefs, hydrothermal vents, and abyssal and hadal habitats, and examine adaptation from the molecular scale to populations, symbiotic associations, and organismal morphology. Together, the studies show how organisms cope with environmental stress through biochemical protection, restructuring of microbial communities, metabolic cooperation, population connectivity, and evolutionary diversification. They also highlight the value of combining complementary approaches to distinguish short-term responses to environmental stress from longer-term evolutionary processes. By bringing together these perspectives, this Research Topic contributes to a broader understanding of how life adapts to extreme marine environments and how the evolutionary and ecological consequences of environmental change may unfold across biological scales.

Responses to environmental stress: from biochemical protection to microbiome restructuring

Environmental stress can be addressed through physiological and biochemical mechanisms that protect organisms from potentially damaging conditions. Hammerle et al. investigated the distribution of mycosporine-like amino acids (MAAs), natural UV-protective compounds, in three species of flatfish from the Baltic Sea. Combining targeted and untargeted metabolomics, they identified several MAAs and found that these compounds accumulated preferentially in the eyes, where concentrations were substantially higher than in other tissues. The detection of MAAs in internal organs also provides evidence for their transfer within the organism and supports the hypothesis that these compounds can be acquired from dietary sources and selectively transported to tissues exposed to ultraviolet radiation. The study further revealed a diversity of MAA-related metabolites, including compounds that may not have been previously characterized. These findings illustrate how the distribution of protective metabolites within an organism can contribute to coping with persistent environmental stress and highlight the potential of metabolomic approaches for uncovering biochemical mechanisms associated with environmental tolerance.

While Hammerle et al. focused on biochemical protection within individual organisms, Pascual-Benito et al. examined responses at the level of the coral holobiont. Their study investigated how thermal stress affects the bacterial microbiomes of soft corals originating from polar, temperate, and tropical environments. By combining field sampling, controlled heat-stress experiments, and 16S rRNA sequencing, the authors showed that each coral species harbored a distinct bacterial community that differed substantially from the surrounding seawater. Experimental warming nevertheless disrupted these host-associated communities, resulting in the reduction of characteristic symbionts and an increase in opportunistic or seawater-associated bacteria. The magnitude of these changes differed among host species: Antarctic and tropical corals showed substantial microbiome restructuring under moderate warming, whereas the Mediterranean species maintained greater stability until exposure to more extreme temperatures. These results demonstrate that the environmental history of host populations can influence the stability of their microbial associations and that thermal stress can rapidly modify interactions within marine holobionts. Together with the findings of Hammerle et al., this study illustrates how organisms can respond to environmental stress through mechanisms operating at different biological levels, from the distribution of protective molecules within tissues to the restructuring of entire microbial communities.

Microbial partnerships and metabolic cooperation in extreme environments

Host-microbe interactions can also provide more direct mechanisms for exploiting environments characterized by strong chemical constraints. Li et al. investigated the microbiome and virome of an undescribed glass sponge collected from a hydrothermal vent field in the Okinawa Trough at a depth of 1,284 m. Metagenomic analyses revealed a diverse microbial community comprising sulfur-oxidizing bacteria, ammonia-oxidizing archaea, methane-oxidizing bacteria, and other microorganisms involved in carbon and nitrogen cycling. The reconstructed microbial genomes indicated complementary metabolic capacities, including sulfur and methane oxidation, carbon fixation, nitrogen transformations, and the degradation of potentially harmful compounds. Such functional diversity suggests that the sponge holobiont can integrate multiple microbial processes in an environment where reduced chemical compounds provide important sources of energy. The study also identified a methane-oxidizing symbiont with genomic characteristics consistent with an early stage of symbiotic genome reduction, providing insight into the evolutionary transition from free-living microorganisms towards more specialized host-associated lifestyles. In addition, the diverse viral community may contribute to regulating microbial populations and recycling nutrients within the holobiont. By revealing interactions among the sponge host, microbial symbionts, and viruses, this study highlights the importance of metabolic cooperation in the functioning of communities exposed to extreme chemical conditions.

Connectivity and evolutionary processes in isolated environments

Adaptation to extreme environments is not restricted to physiological or biochemical responses, but can also involve population-level processes that determine how organisms persist and evolve across fragmented habitats. [Prófumo et al.](#) examined population connectivity in the Antarctic isopod *Spinoserolis beddardi*, a species that lacks a pelagic larval stage and might therefore be expected to exhibit limited dispersal among populations. Using nearly 14,000 genome-wide SNPs from individuals collected at three coastal sites on Livingston Island, the authors found remarkably low genetic differentiation among populations separated by 2–13 km. The results indicate substantial genetic connectivity despite the species' life-history characteristics, suggesting that occasional dispersal through oceanographic transport, together with shared evolutionary history, may contribute to maintaining gene flow among populations. This study emphasizes that dispersal and connectivity can persist even in species with limited opportunities for active long-distance movement and illustrates how population genomic approaches can reveal evolutionary processes that are not readily apparent from life-history traits alone. Understanding such processes is particularly relevant in extreme environments, where the persistence of populations may depend not only on physiological tolerance but also on their capacity to remain connected across spatially heterogeneous habitats.

Morphological diversification and evolutionary novelty in the deep sea

The deep sea provides another perspective on how evolution can generate diversity under environmental conditions that remain comparatively poorly explored. [González-Casarrubios et al.](#) describe two new species of deep-sea kinorhynchs, *Echinoderes prior* and *Echinoderes shimadai*, collected from abyssal and hadal environments in the Pacific Ocean. Both species possess a middorsal spine on trunk segment 9, a feature that extends beyond the segment range traditionally considered characteristic of this morphological group. Integrating detailed morphological observations with mitochondrial COI and nuclear 18S and 28S markers, the authors confirmed the distinctiveness of the two species and identified additional genetic diversity within *E. prior*. Phylogenetic analyses suggest that the segment 9 spine was secondarily reacquired within the lineage, while observations of post-embryonic development showed that posterior spines can be added or lost during successive molts. These findings indicate that morphological characters used in the taxonomy of deep-sea kinorhynchs can be more evolutionarily dynamic than previously assumed. More broadly, the discovery of new species and previously unrecognized morphological and genetic variation in abyssal and hadal environments underscores how much evolutionary diversity remains to be documented in the deep sea.

Taken together, the contributions to this Research Topic illustrate that adaptation and evolution in extreme marine

environments operate across multiple levels of biological organization. Responses to environmental stress may involve the accumulation and redistribution of protective metabolites, changes in host-associated microbial communities, or metabolic cooperation among hosts, bacteria, archaea, and viruses. At broader evolutionary scales, population connectivity can influence the persistence of geographically separated populations, while changes in morphology and development can contribute to diversification and the emergence of new evolutionary traits.

The studies gathered here also demonstrate the value of combining complementary approaches to understand these processes. Metabolomics, controlled experiments, microbiome and metagenomic analyses, population genomics, phylogenetics, and detailed morphological observations each provide access to different components of adaptation and evolution ([Thangaraj and Sun, 2025](#)). Their integration is particularly important in extreme environments, where ecological processes and evolutionary histories can be difficult to disentangle from observations at a single scale ([Burraco et al., 2025](#)). As technological and methodological advances continue to expand access to these habitats, they will provide new opportunities to investigate how organisms and their associated communities respond to environmental challenges and how these responses contribute to the generation and maintenance of marine biodiversity.

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Conflict of interest

The author(s) declared that this work was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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References

- Avila, C., Taboada, S., and Núñez-Pons, L. (2008). Antarctic marine chemical ecology: what is next? *Mar. Ecol.* 29, 1–71. doi: 10.1111/j.1439-0485.2007.00215.x
- Burraco, P., Hawkes, L., Pilakouta, N., Angelier, F., Brans, K. I., and Orizaola, G. (2025). Evolutionary ecophysiology in extreme environments under a global change scenario. *Conserv. Physiol.* 13, coaf059. doi: 10.1093/conphys/coaf059
- Guo, Y., Wang, Z., Li, D., Wang, L., Lan, H., Guo, F., et al. (2026). The genetic repertoire of deep-sea microbiome: From sequence to structure and function. *Cell. Host Microbe* 34, 1509–1522.e10. doi: 10.1016/j.chom.2026.05.009
- Hourdez, S., and Lallier, F. H. (2007). Adaptations to hypoxia in hydrothermal-vent and cold-seep invertebrates. *Rev. Environ. Sci. Bio/Technol.* 6, 143–159. doi: 10.1007/s11157-006-9110-3
- Minic, Z. (2009). Organisms of deep sea hydrothermal vents as a source for studying adaptation and evolution. *Symbiosis* 47, 121–132. doi: 10.1007/BF03179972
- Núñez-Pons, L., Avila, C., Romano, G., Verde, C., and Giordano, D. (2018). UV-protective compounds in marine organisms from the southern ocean. *Mar. Drugs* 16, 336. doi: 10.3390/md16090336
- Parrilli, E., Tedesco, P., Fondi, M., Tutino, M. L., Lo Giudice, A., de Pascale, D., et al. (2021). The art of adapting to extreme environments: The model system *Pseudalteromonas*. *Phys. Life Rev.* 36, 137–161. doi: 10.1016/j.plrev.2019.04.003
- Peck, L. S. (2018). “Antarctic marine biodiversity: Adaptations, environments and responses to change,” in *Oceanography and Marine Biology: An Annual Review*, vol. 56. Eds. S. J. Hawkins, A. J. Evans, A. C. Dale, L. B. Firth and I. P. Smith (Boca Raton, FL: CRC Press), 105–236. doi: 10.1201/9780429454455-3
- Pita, L., Rix, L., Slaby, B. M., Franke, A., and Hentschel, U. (2018). The sponge holobiont in a changing ocean: from microbes to ecosystems. *Microbiome* 6, 46. doi: 10.1186/s40168-018-0428-1
- Saeedi, H. (2026). Gaps and drivers of global marine animal biodiversity from the surface to abyss. *Nat. Commun.* 17, 4553. doi: 10.1038/s41467-026-73613-z
- Sánchez, O., Stefanni, S., and Bhadury, P. (2024). The deep sea biodiversity and conservation collection. *Sci. Rep.* 14, 27559. doi: 10.1038/s41598-024-77742-7
- Smith, K. E., Sen Gupta, A., Burrows, M. T., Filbee-Dexter, K., Hobday, A. J., Holbrook, N. J., et al. (2025). Ocean extremes as a stress test for marine ecosystems and society. *Nature Climate Change* 15 (3), 231–235. doi: 10.1038/s41558-025-02269-2
- Thangaraj, S., and Sun, J. (2025). Omics insights into ocean health: Molecular adaptations and ecosystem resilience under climate stress. *Adv. Clim. Change Res.* 17, 199–217. doi: 10.1016/j.accre.2025.10.004

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